

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lawrence, Geoffrey
- (ii) TITLE OF THE INVENTION: Novel Compounds
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Ratner & Prestia
 - (B) STREET: P.O. Box 980
 - (C) CITY: Valley Forge
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19482
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 96 24677.2
 - (B) FILING DATE: Filed November 27, 1996
and
 - (A) APPLICATION NUMBER: GB 9709463.5
 - (B) FILING DATE: May 9, 1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Prestia, Paul F.
 - (B) REGISTRATION NUMBER: 23,031
 - (C) REFERENCE/DOCKET NUMBER: GH30170
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 610-407-0700
 - (B) TELEFAX: 610-407-0701
 - (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

08977862.1.2597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCCGCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGCTGCC	180
TACCACCACC	TGGATTCTTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCGCAT	GAAGAACCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCCC	GCAGCCTTGG	TAACATATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
CTGCCGCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGGA	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAGCAA	TGTCAACACC	AGTGTTCCTT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGAACCC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
CCACACCCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25				30			
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
		35				40					45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
	50					55					60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70					75				80	
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
			85					90						95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
		100						105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
	115					120					125				
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130					135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145				150						155				160	
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
			165					170					175		
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
		180						185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala

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	195		200		205										
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
	210						215				220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Asn	Thr	Ile		Ala	Pro	Asn	Cys	Ala
	225				230				235						240
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
			245						250						255
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
			260						265				270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
			275				280						285		
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
	290						295						300		
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
	305				310						315				320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
			325						330						335
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
			340						345				350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
			355				360						365		
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
	370						375						380		
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
	385				390						395				400

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTGC GCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCACACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCACCTTG	CAGTGATGCC	180
TACCACCACC	TGGATTCCTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCGCAT	GAAGAACCAG	GTTCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCCC	GCAGCCTTGG	TAATATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
CTGCCGCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGGA	TTTCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAACAA	TGTCAACACC	AGTGTTCCT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
CCACACCCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:4:

00977862-112597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25					30		
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
		35					40					45			
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Asp	Ala	Tyr	His	His	Leu
	50					55				60					
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70					75					80
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
				85					90					95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
			100					105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
		115					120					125			
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130					135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145					150					155					160
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
			165						170					175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180					185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
		195					200					205			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
	210					215					220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
225					230					235					240
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
			245						250					255	
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
		260						265					270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
		275					280					285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
	290					295					300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
305					310					315					320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
			325						330					335	
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
			340					345					350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
		355					360					365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
	370					375					380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp

08977862-112597

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GAGCGCCGGC GCAACACCAT CGCCCCAAC TGC GCGCTGC CGCCTGTGGC CCCC AACTGC      60
CTGGAGCTGC GCGCCTCTG CTTCTCCGAC CCGCTTTGCA GATCACGCCT GGTGGATTTC      120
CAGACCCACT GCCATCCCAT GGACATCCTA GGAAC TTGTG CAACAGAGCA GTCCAGATGT      180
CTACGAGCAT ACCTGGGGCT GATTGGGACT GCCATGACCC CCAACTTTGT CAGCAATGTC      240
AACACCAGTG TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT      300
GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT TGCAGCTAAG      360
ATGCGTTTTT ACAGCCAACT CTTCTCCCAG GACTGGCCAC ACCCTACCTT TGCTGTGATG      420
GCACACCAGA ATGAAAACCC TGCTGTGAGG CCACAGCCCT GGGTGCCCTC TCTTTTCTCC      480
TGCACGCTTC CCTTGATTCT GCTCCTGAGC CTATGGTAG                               519

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala Leu Pro Pro Val
 1           5           10           15
Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe Ser Asp Pro Leu
           20           25           30
Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys His Pro Met Asp
           35           40           45
Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr
           50           55           60
Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Val Ser Asn Val
           65           70           75           80
Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu
           85           90           95
Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser His Asn Pro Cys
           100          105          110
Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His Ser Gln Leu Phe
           115          120          125
Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala His Gln Asn
           130          135          140
Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser Leu Phe Ser
           145          150          155          160
Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
           165          170

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08977862.112597

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lawrence, Geoffrey
- (ii) TITLE OF THE INVENTION: Novel Compounds
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Ratner & Prestia
 - (B) STREET: P.O. Box 980
 - (C) CITY: Valley Forge
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19482
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 96 24677.2
 - (B) FILING DATE: Filed November 27, 1996
and
 - (A) APPLICATION NUMBER: GB 9709463.5
 - (B) FILING DATE: May 9, 1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Prestia, Paul F.
 - (B) REGISTRATION NUMBER: 23,031
 - (C) REFERENCE/DOCKET NUMBER: GH30170
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 610-407-0700
 - (B) TELEFAX: 610-407-0701
 - (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

00977862-112597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGCGCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TCCCCACAGA	AAGCCGACTC	120
ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCCACCTG	CAGTGCTGCC	180
TACCACCACC	TGGATTCTTG	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
TGCATGTGCC	ACCGGCGCAT	GAAGAACCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
CACCGTGCCC	GCAGCCTTGG	TAACATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
CTGCCGCCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
TGCAGATCAC	GCCTGGTGGA	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
ACCCCCAACT	TTGTCAACAA	TGTCAACACC	AGTGTTCCTT	TAAGCTGCAC	CTGCCGAGGC	960
AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
CTCACGGAGG	CCATTGCAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
CCACACCCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25				30			
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
		35					40				45				
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
	50				55					60					
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70				75					80	
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
			85					90						95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
		100					105					110			
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
	115					120					125				
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130				135					140					
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145				150					155					160	
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
			165					170						175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180				185					190			
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala

08977862 " 112597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1 5 10 15
Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20 25 30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35 40 45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu
50 55 60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65 70 75 80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85 90 95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
100 105 110
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
115 120 125
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130 135 140
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145 150 155 160
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165 170 175
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
180 185 190
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
195 200 205
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
210 215 220
Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
225 230 235 240
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
245 250 255
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
260 265 270
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
275 280 285
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
290 295 300
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
305 310 315 320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
325 330 335
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
340 345 350
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
355 360 365
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
370 375 380
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp

08977862.112597

385

390

395

400

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCGCCGGC	GCAACACCAT	CGCCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTTGCA	GATCACGCCT	GGTGGATTTC	120
CAGACCCACT	GCCATCCCAT	GGACATCCTA	GGAACCTGTG	CAACAGAGCA	GTCCAGATGT	180
CTACGAGCAT	ACCTGGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTTGT	CAGCAATGTC	240
AACACCAGTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGAGTGT	300
GAAATGCTGG	AAGGGTTCTT	CTCCCACAAC	CCCTGCCTCA	CGGAGGCCAT	TGCAGCTAAG	360
ATGCGTTTTT	ACAGCCAACT	CTTCTCCAG	GACTGGCCAC	ACCCTACCTT	TGCTGTGATG	420
GCACACCAGA	ATGAAAACCC	TGCTGTGAGG	CCACAGCCCT	GGGTGCCCTC	TCTTTTCTCC	480
TGCACGCTTC	CCTTGATTCT	GCTCCTGAGC	CTATGGTAG			519

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	
1				5					10					15		
Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu	
			20					25					30			
Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	
		35					40					45				
Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	
	50					55					60					
Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val	
65					70					75					80	
Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	
			85						90					95		
Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys	
			100					105					110			
Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe	
		115				120						125				
Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn	
	130					135					140					
Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser	
145					150					155					160	
Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp					
				165							170					

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Figure 1 - SEQ ID NO:1

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
 101 TTCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
 151 TGCCAGGCTG ATCCACCTG CAGTGCTGCC TACCACCACC TGGATTCCTG
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCTGCT TGGACATCTA
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
 401 CCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
 451 AAAGTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
 501 GCTGTGTA CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG
 601 CTCACCTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
 701 CCATCGCCCC CAACTGCGCG CTGCCGCTG TGGCCCCCAA CTGCCTGGAG
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAACT TGTGCAACAG
 851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
 901 ACCCCCCA ACT TTGTCAGCAA TGTCAACACC AGTGTTGCCT TAAGCTGCAC
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCTA CCTTTGCTGT
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

Figure 2 - SEQ ID NO:2

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 51 CQADPTCSAA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
 101 CMCHRRMKNQ VACLDIYWTV HRARSLGNYE LDVSPYEDTV TSKPWKMNLS
 151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCLE
 251 LRRLCFSDPL CRSRLVDFQT HCHPMDILGT CATEQSRCLR AYLGLIGTAM
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
 351 FHSQLFSDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

Figure 3 - SEQ ID NO:3

1 ATGGTGC GCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
 101 TTCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
 151 TGCCAGGCTG ATCCACCTG CAGTGATGCC TACCACCACC TGGATTCCTG
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
 401 CCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
 451 AAAGTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG
 601 CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
 701 CCATCGCCCC CAACTGCGCG CTGCCGCTG TGGCCCCCAA CTGCCTGGAG
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGG
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC TGTGCAACAG
 851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
 901 ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTTCCT TAAGCTGCAC
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
 1001 TCTTCTCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCTA CCTTTGCTGT
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

Figure 4 - SEQ ID NO:4

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 51 CQADPTCSDA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
 101 CMCHRRMKNQ VACLDIYWTV HRARSLGNYE LDVSPYEDTV TSKPWKMNLS
 151 KLNMLKPDSD LCLKFAMLC LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCLE
 251 LRRLCFSDPL CRSRLVDFQT HCHPMDILGT CATEQSRCLR AYLGLIGTAM
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
 351 FHSQLFSQDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

Figure 5 - SEQ ID NO:5 (Partial coding cDNA sequence for human GDNF α 3 receptor)

1 GAGCGCCGGC GCAACACCAT CGCCCCAAC TGC GCGCTGC CGCCTGTGGC
5 51 CCCCAACTGC CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTTGCA
101 GATCACGCCT GGTGGATTTC CAGACCCACT GCCATCCCAT GGACATCCTA
10 151 GGA ACTTGTG CAACAGAGCA GTCCAGATGT CTACGAGCAT ACCTGGGGCT
201 GATTGGGACT GCCATGACCC CCAACTTTGT CAGCAATGTC AACACCAAGTG
251 TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT
15 301 GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT
351 TGCAGCTAAG ATGCGTTTTTC ACAGCCAACT CTTCTCCCAG GACTGGCCAC
20 401 ACCCTACCTT TGCTGTGATG GCACACCAGA ATGAAAACCC TGCTGTGAGG
451 CCACAGCCCT GGGTGCCCTC TCTTTTCTCC TGCACGCTTC CCTTGATTCT
501 GCTCCTGAGC CTATGGTAG

Figure 6 - SEQ ID NO:6 (amino acid sequence for the partial GDNF α 3 receptor sequence)

1 ERRRNTIAPN CALPPVAPNC LELRRLCFSD PLCRSRLVDF QTHCHPMDIL
30 51 GTCATEQSRC LRAYLGLIGT AMTPNEFSNV NTSVALSCTC RGSGNLQEEC
101 EMLEGFFSHN PCLTEAIAAK MRFHSQ LFSQ DWPHTFAVM AHQENPAVR
35 151 PQPWVPSLFS CTLPLILLLS LW

The sequence underlined corresponds to the predicted hydrophobic C-terminus characteristic of GPI anchored cell-surface receptors

Figure 1 - SEQ ID NO:1

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
 101 TTCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
 151 TGCCAGGCTG ATCCACCTG CAGTGCTGCC TACCACCACC TGGATTCCCTG
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
 401 CCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
 451 AAAGTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG
 601 CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
 701 CCATCGCCCC CAACTGCGCG CTGCCGCTG TGGCCCCAA CTGCCTGGAG
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAGT TGTGCAACAG
 851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
 901 ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTTCCT TAAGCTGCAC
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
 1051 TTTCACAGCC AACTCTTCTC CCAGGACTGG CCACACCCTA CCTTTGCTGT
 1101 GATGGCACAC CAGAAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
 1151 CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

Figure 2 - SEQ ID NO:2

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 51 CQADPTCSAA YHHLDSCTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
 101 CMCHRRMKNQ VACLDIYWTV HRARSLGNYE LDVSPYEDTV TSKPWKMNLS
 151 KLNMLKPDSD LCLKFAMLCT LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCLE
 251 LRRLCFSDPL CRSRLVDFQT HCHPMDILGT CATEQSRCLR AYLGLIGTAM
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTAIAAKMR
 351 FHSQLFSDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

Figure 3 - SEQ ID NO:3

1 ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT
 51 GCTGCTGCTG CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC
 101 TTCCACAGA AAGCCGACTC ATGAACAGCT GTCTCCAGGC CAGGAGGAAG
 151 TGCCAGGCTG ATCCACCTG CAGTGATGCC TACCACCACC TGGATTCCTG
 201 CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT TCGGTCCCTG
 251 CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC
 301 TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA
 351 TTGGACCGTT CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT
 401 CCCCCTATGA AGACACAGTG ACCAGCAAAC CCTGGAAAAT GAATCTCAGC
 451 AAAGTGAACA TGCTCAAACC AGACTCAGAC CTCTGCCTCA AGTTTGCCAT
 501 GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG GCCTACGGGG
 551 AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG
 601 CTCACCTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT
 651 GTGCCCATGT GCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA
 701 CCATCGCCCC CAACTGCGCG CTGCCGCTG TGGCCCCCAA CTGCCTGGAG
 751 CTGCGGCGCC TCTGCTTCTC CGACCCGCTT TGCAGATCAC GCCTGGTGGA
 801 TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAT TGTGCAACAG
 851 AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG
 901 ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTGCCT TAAGCTGCAC
 951 CTGCCGAGGC AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT
 1001 TCTTCTCCCA CAACCCCTGC CTCACGGAGG CCATTGCAGC TAAGATGCGT
 1051 TTTACAGACC AACTCTTCTC CCAGGACTGG CCACACCCTA CCTTTGCTGT
 1101 GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG CCCTGGGTGC
 1151 CCTCTTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG

Figure 4 - SEQ ID NO:4

1 MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 51 CQADPTCSDA YHLDSTSS ISTPLPSEEP SVPADCLEAA QQLRNSSLIG
 101 CMCHRRMKNQ VACLDIYWTV HRARSLGNYE LDVSPYEDTV TSKPWKMNLS
 151 KLNMLKPDSD LCLKFAMLC LNDKCDRLRK AYGEACSGPH CQRHVCLRQL
 201 LTFFEKAAEP HAQGLLLCPC APNDRGCGER RRNTIAPNCA LPPVAPNCLE
 251 LRRLCFSDPL CRSRLVDFQT HCHPMDILGT CATEQSRCLR AYLGLIGTAM
 301 TPNFVSNVNT SVALSCTCRG SGNLQEECEM LEGFFSHNPC LTEAIAAKMR
 351 FHSQLFSDW PHPTFAVMAH QNENPAVRPQ PWVPSLFSCT LPLILLLSLW

Figure 5 - SEQ ID NO:5 (Partial coding cDNA sequence for human GDNF α 3 receptor)

1 GAGCGCCGGC GCAACACCAT CGCCCCAAC TGC GCGCTGC CGCCTGTGGC
5 51 CCCCAACTGC CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTTGCA
101 GATCACGCCT GGTGGATTTC CAGACCCACT GCCATCCCAT GGACATCCTA
10 151 GGA ACTTGTG CAACAGAGCA GTCCAGATGT CTACGAGCAT ACCTGGGGCT
201 GATTGGGACT GCCATGACCC CCAACTTTGT CAGCAATGTC AACACCAGTG
251 TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT
15 301 GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT
351 TGCAGCTAAG ATGCGTTTTT ACAGCCAACT CTTCTCCCAG GACTGGCCAC
20 401 ACCCTACCTT TGCTGTGATG GCACACCAGA ATGAAAACCC TGCTGTGAGG
451 CCACAGCCCT GGGTGCCCTC TCTTTTCTCC TGCACGCTTC CCTTGATTCT
501 GCTCCTGAGC CTATGGTAG
25

Figure 6 - SEQ ID NO:6 (amino acid sequence for the partial GDNF α 3 receptor sequence)

1 ERRRNTIAPN CALPPVAPNC LELRRLCFSD PLCRSRLVDF QTHCHPMDIL
30 51 GTCATEQSRC LRAYLGLIGT AMTPNFVSNV NTSVALSCTC RGSGNLQEEC
101 EMLEGFFSHN PCLTEAIAAK MRFHSQLFSQ DWPHPTFAVM AHQENPAVR
35 151 PQPWVPSLFS CTLPLILLLS LW

The sequence underlined corresponds to the predicted hydrophobic C-terminus characteristic of GPI anchored cell-surface receptors